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SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

(ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-12

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson

(B) STREET: 4225 Executive Square, Suite 1400

(C) CITY: La Jolla

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/US95/

(B) FILING DATE: 12-JUL-1995

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Haile, Ph.D., Lisa A

(B) REGISTRATION NUMBER: 38,347

(C) REFERENCE/DOCKET NUMBER: 07265/042WO1 (FD-3830)

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-678-5070

(B) TELEFAX: 619-678-5099

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

RHS
51

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Modified Base

(B) LOCATION: 12...12

(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base

(B) LOCATION: 26...26

(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base

(B) LOCATION: 29...29

(D) OTHER INFORMATION: Inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGAATTCG GNTGGMGNVA TGGRTNRTNT AYCC

34

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Modified Base

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(B) LOCATION: 13...13
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY:Modified Base
(B) LOCATION: 19...19
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY:Modified Base
(B) LOCATION: 25...25
(D) OTHER INFORMATION: Inosine; Inosine also at position
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCTC CANSRCANC YNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY:Modified Base
(B) LOCATION: 19...19
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY:Modified Base
(B) LOCATION: 25...25
(D) OTHER INFORMATION: Inosine; Inosine also at position
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGAATTCT CANSRCANT SNYGNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

15

(A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

20

(A) NAME/KEY: Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

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(A) NAME/KEY: Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position

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ORIGINAL SOURCE

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGAATTCT CANSCRCANT SNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

- (A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(D) OTHER INFORMATION: Inosine

- (A) NAME/KEY: Modified Base
(B) LOCATION: 19...19
(D) OTHER INFORMATION: Inosine

- (A) NAME/KEY: Modified Base
(B) LOCATION: 25...25
(D) OTHER INFORMATION: Inosine; Inosine also at position
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGAATTCT CANSCRCANT SNBTNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCT CANSRCANG MNYGNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

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(A) NAME/KEY:Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGGAATTCT CANS~~C~~RCANG MNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: ~~nucleic~~ acid

(C) STRANDEDNESS \ single

(D) TOPOLOGY: ~~linear~~

(ii) MOLECULE TYPE: ~~cDNA~~

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) **FRAGMENT TYPE:**

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

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(A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

25

(A) NAME/KEY:Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

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(A) NAME/KEY:Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGAATTCT CANSRCANM GNYGNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:9:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 19...19
(D) OTHER INFORMATION: Inosine

(A) NAME/KEY: Modified Base
(B) LOCATION: 25...25
(D) OTHER INFORMATION: Inosine; Inosine also at position
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGGAATTCT CAnSCRCANM GNWCNACNMY CAT

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(A) NAME/KEY: Modified Base
(B) LOCATION: 13...13
(D) OTHER INFORMATION: Inosine

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(A) NAME/KEY: Modified Base
 (B) LOCATION: 19...19
 (D) OTHER INFORMATION: Inosine

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(A) NAME/KEY: Modified Base
 (B) LOCATION: 25...25
 (D) OTHER INFORMATION: Inosine; Inosine also at position
 28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCGGAATTCTC CANSRCANM GNWCNACNMY CAT

33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

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(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

25

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...357

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30

CGG GCC AGG AGG AGG ACC CCC ACC TGT GAG CCT GCG ACC CCC TTA TGT
 Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys
 1 5 10 15

48

TGC AGG CGA GAC CAT TAC GTA GAC TTC CAG GAA CTG GGA TGG CGG GAC
 Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp
 20 25 30

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TGG ATA CTG CAG CCC GAG GGG TAC CAG CTG AAT TAC TGC AGT GGG CAG
 Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln
 35 40 45

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TGC CCT CCC CAC CTG GCT GGC AGC CCA GGC ATT GCT GCC TCT TTC CAT 192
 Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His
 50 55 60

TCT GCC GTC TTC AGC CTC CTC AAA GCC AAC AAT CCT TGG CCT GCC AGT 240
 Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser
 65 70 75 80

ACC TCC TGT TGT GTC CCT ACT GCC CGA AGG CCC CTC TCT CTC CTC TAC 288
 Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr
 85 90 95

CTG GAT CAT AAT GGC AAT GTG GTC AAG ACG GAT GTG CCA GAT ATG GTG 336
 Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val
 100 105 110

GTG GAG GCC TGT GGC TGC AGC TAG 360
 Val Glu Ala Cys Gly Cys Ser
 115

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys
 1 5 10 15

Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp
 20 25 30

Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln
 35 40 45

Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His
 50 55 60

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Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser
 65 70 75 80
 Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr
 85 90 95
 5 Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val
 100 105 110
 Val Glu Ala Cys Gly Cys Ser
 115

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 218...1267

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCTGTGAG GGTCAAGCAC AGCTATCCAT CAGATGATCT ACTTTCAGCC TTCCTGAGTC 60
 CCAGACAATA GAAGACAGGT GGCTGTACCC TTGGCCAAGG GTAGGTGTGG CAGTGGTGTC 120
 TGCTGTCACT GTGCCCTCAT TGGCCCCCAG CAATCAGACT CAACAGAAGG AGCAACTGCC 180
 ATCCGAGGCT CCTGAACCAG GGCCATTAC CAGGAGC ATG CGG CTC CCT GAT GTC 235
 Met Arg Leu Pro Asp Val
 1 5
 CAG CTC TGG CTG GTG CTG CTG TGG GCA CTG GTG CGA GCA CAG GGG ACA 283
 Gln Leu Trp Leu Val Leu Leu Trp Ala Leu Val Arg Ala Gln Gly Thr
 10 15 20

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GGG TCT GTG TGT CCC TCC TGT GGG GGC TCC AAA CTG GCA CCC CAA GCA 331
 Gly Ser Val Cys Pro Ser Cys Gly Gly Ser Lys Leu Ala Pro Gln Ala
 25 30 35

5 GAA CGA GCT CTG GTG CTG GAG CTA GCC AAG CAG CAA ATC CTG GAT GGG 379
 Glu Arg Ala Leu Val Leu Glu Leu Ala Lys Gln Gln Ile Leu Asp Gly
 40 45 50

TTG CAC CTG ACC AGT CGT CCC AGA ATA ACT CAT CCT CCA CCC CAG GCA 427
 Leu His Leu Thr Ser Arg Pro Arg Ile Thr His Pro Pro Pro Gln Ala
 55 60 65 70

10 GCG CTG ACC AGA GCC CTC CGG AGA CTA CAG CCA GGG AGT GTG GCT CCA 475
 Ala Leu Thr Arg Ala Leu Arg Arg Leu Gln Pro Gly Ser Val Ala Pro
 75 80 85

GGG AAT GGG GAG GAG GTC ATC AGC TTT GCT ACT GTC ACA GAC TCC ACT 523
 Gly Asn Gly Glu Glu Val Ile Ser Phe Ala Thr Val Thr Asp Ser Thr
 15 90 95 100

TCA GCC TAC AGC TCC CTG CTC ACT TTT CAC CTG TCC ACT CCT CGG TCC 571
 Ser Ala Tyr Ser Ser Leu Leu Thr Phe His Leu Ser Thr Pro Arg Ser
 105 110 115

CAC CAC CTG TAC CAT GCC CGC CTG TGG CTG CAC GTG CTC CCC ACC CTT 619
 His His Leu Tyr His Ala Arg Leu Trp Leu His Val Leu Pro Thr Leu
 20 120 125 130

CCT GGC ACT CTT TGC TTG AGG ATC TTC CGA TGG GGA CCA AGG AGG AGG 667
 Pro Gly Thr Leu Cys Leu Arg Ile Phe Arg Trp Gly Pro Arg Arg Arg
 135 140 145 150

CGC CAA GGG TCC CGC ACT CTC CTG GCT GAG CAC CAC ATC ACC AAC CTG 715
 Arg Gln Gly Ser Arg Thr Leu Leu Ala Glu His His Ile Thr Asn Leu
 155 160 165

GGC TGG CAT ACC TTA ACT CTG CCC TCT AGT GGC TTG AGG GGT GAG AAG 763
 Gly Trp His Thr Leu Thr Leu Pro Ser Ser Gly Leu Arg Gly Glu Lys
 30 170 175 180

TCT GGT GTC CTG AAA CTG CAA CTA GAC TGC AGA CCC CTA GAA GGC AAC 811
 Ser Gly Val Leu Lys Leu Gln Leu Asp Cys Arg Pro Leu Glu Gly Asn
 185 190 195

AGC ACA GTT ACT GGA CAA CCG AGG CGG CTC TTG GAC ACA GCA GGA CAC 859
 Ser Thr Val Thr Gly Gln Pro Arg Arg Leu Leu Asp Thr Ala Gly His
 35 200 205 210

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CAG CAG CCC TTC CTA GAG CTT AAG ATC CGA GCC AAT GAG CCT GGA GCA 907
 Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg Ala Asn Glu Pro Gly Ala
 215 220 225 230

GGC CGG GCC AGG AGG AGG ACC CCC ACC TGT GAG CCT GCG ACC CCC TTA 955
 Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu
 235 240 245

TGT TGC AGG CGA GAC CAT TAC GTA GAC TTC CAG GAA CTG GGA TGG CGG 1003
 Cys Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg
 250 255 260

GAC TGG ATA CTG CAG CCC GAG GGG TAC CAG CTG AAT TAC TGC AGT GGG 1051
 Asp Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly
 265 270 275

CAG TGC CCT CCC CAC CTG GCT GGC AGC CCA GGC ATT GCT GCC TCT TTC 1099
 Gln Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe
 280 285 290

CAT TCT GCC GTC TTC AGC CTC CTC AAA GCC AAC AAT CCT TGG CCT GCC 1147
 His Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala
 295 300 305 310

AGT ACC TCC TGT TGT GTC CCT ACT GCC CGA AGG CCC CTC TCT CTC CTC 1195
 Ser Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu
 315 320 325

TAC CTG GAT CAT AAT GGC AAT GTG GTC AAG ACG GAT GTG CCA GAT ATG 1243
 Tyr Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met
 330 335 340

GTG GTG GAG GCC TGT GGC TGC AGC TAGCAAGAGG ACCTGGGGCT TTGGAGTGAA G 1298
 Val Val Glu Ala Cys Gly Cys Ser
 345 350

AGACCAAGAT GAAGTTTCCC AGGCACAGGG CATCTGTGAC TGGAGGCATC AGATTCTGA 1358

TCCACACCCC AACCCAACAA CCACCTGGCA ATATGACTCA CTTGACCCT ATGGGACCCA 1418

AATGGGCACT TTCTTGCTG AGACTCTGGC TTATTCCAGG TTGGCTGATG TGTTGGGAGA 1478

TGGGTAAAGC GTTTCTTCTA AAGGGGTCTA CCCAGAAAGC ATGATTTCCT GCCCTAAGTC 1538

CTGTGAGAAG ATGTCAGGGA CTAGGGAGGG AGGGAGGGAA GGCAGAGAAA AATTACTTAG 1598

CCTCTCCCAA GATGAGAAAG TCCTCAAGTG AGGGGAGGAG GAAGCAGATA GATGGTCCAG 1658

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CAGGCTTGAA GCAGGGTAAG CAGGCTGGCC CAGGGTAAGG GCTGTTGAGG TACCTTAAGG 1718

GAAGGTCAAG AGGGAGATGG GCAAGGCGCT GAGGGAGGAT GCTTAGGGGA CCCCCAGAAA 1778

CAGGAGTCAG GAAAATGAGG CACTAAGCCT AAGAAGTTCC CTGGTTTTC CCAGGGGACA 1838

GGACCCACTG GGAGACAAGC ATTTATACTT TCTTTCTTCT TTTTATTTT TTTGAGATCG 1898

AGTCTCGCTC TGTCACCAGG CTGGAGTGCA GTGACACGAT CTTGGCTCAC TGCAACCTCC 1958

GTCTCCTGGG TTCAAGTGAT TCTTCTGCCT CAGCCTCCCG AGCAGCTGGG ATTACAGGCG 2018

CCCACTAATT TTTGTATTCT TAGTAGAAAC GAGGTTTCAA CATGTTGGCC AGGATGGTCT 2078

CAATCTCTTG ACCTCTTGAT CCACCCGACT TGGCCTCCCG AAGTGATGAG ATTATAGGCG 2138

TGAGCCACCG CGCCTGGCTT ATACTTTCTT AATAAAAAGG AGAAAGAAAA TCAACAAATG 2198

TGAGTCATAA AGAAGGGTTA GGGTGATGGT CCAGAGCAAC AGTTCTTCAA GTGTACTCTG 2258

TAGGCTTCTG GGAGGTCCCT TTTCAGGGGT GTCCACAAAG TCAAAGCTAT TTTCATAATA 2318

ATACTAACAT GTTATTTGCC TTTTGAATTC TCATTACTT AAAATTGTAT TGTGGAGTTT 2378

TCCAGAGGCC GTGTGACATG TGATTACATC ATCTTTCTGA C 2419

(2) INFORMATION FOR SEQ ID NO:14:

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Leu Pro Asp Val Gln Leu Trp Leu Val Leu Leu Trp Ala Leu
1 5 10 15

Val Arg Ala Gln Gly Thr Gly Ser Val Cys Pro Ser Cys Gly Gly Ser
20 25 30

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Lys Leu Ala Pro Gln Ala Glu Arg Ala Leu Val Leu Glu Leu Ala Lys
 35 40 45

Gln Gln Ile Leu Asp Gly Leu His Leu Thr Ser Arg Pro Arg Ile Thr
 50 55 60

His Pro Pro Pro Gln Ala Ala Leu Thr Arg Ala Leu Arg Arg Leu Gln
 65 70 75 80

Pro Gly Ser Val Ala Pro Gly Asn Gly Glu Glu Val Ile Ser Phe Ala
 85 90 95

10

Thr Val Thr Asp Ser Thr Ser Ala Tyr Ser Ser Leu Leu Thr Phe His
 100 105 110

Leu Ser Thr Pro Arg Ser His His Leu Tyr His Ala Arg Leu Trp Leu
 115 120 125

His Val Leu Pro Thr Leu Pro Gly Thr Leu Cys Leu Arg Ile Phe Arg
 130 135 140

15

Trp Gly Pro Arg Arg Arg Arg Gln Gly Ser Arg Thr Leu Leu Ala Glu
 145 150 155 160

His His Ile Thr Asn Leu Gly Trp His Thr Leu Thr Leu Pro Ser Ser
 165 170 175

Gly Leu Arg Gly Glu Lys Ser Gly Val Leu Lys Leu Gln Leu Asp Cys
 180 185 190

20

Arg Pro Leu Glu Gly Asn Ser Thr Val Thr Gly Gln Pro Arg Arg Leu
 195 200 205

Leu Asp Thr Ala Gly His Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg
 210 215 220

25

Ala Asn Glu Pro Gly Ala Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys
 225 230 235 240

Glu Pro Ala Thr Pro Leu Cys Cys Arg Arg Asp His Tyr Val Asp Phe
 245 250 255

30

Gln Glu Leu Gly Trp Arg Asp Trp Ile Leu Gln Pro Glu Gly Tyr Gln
 260 265 270

Leu Asn Tyr Cys Ser Gly Gln Cys Pro Pro His Leu Ala Gly Ser Pro
 275 280 285

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Gly Ile Ala Ala Ser Phe His Ser Ala Val Phe Ser Leu Leu Lys Ala
290 295 300

Asn Asn Pro Trp Pro Ala Ser Thr Ser Cys Cys Val Pro Thr Ala Arg
305 310 315 320

Arg Pro Leu Ser Leu Leu Tyr Leu Asp His Asn Gly Asn Val Val Lys
325 330 335

Thr Asp Val Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser
340 345 350

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